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OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/970,076

DATE: 10/24/2001
TIME: 14:17:42

Input Set : A:\Uw977451.app
Output Set: N:\CRF3\10242001\I970076.raw

3 <110> APPLICANT: Young, John A.T.
4 Bradley, Kenneth A.
5 Collier, Robert J.
6 Mogridge, Jeremy S.
8 <120> TITLE OF INVENTION: Anthrax Toxin Receptor
10 <130> FILE REFERENCE: 960296.97745
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/970,076 OVR
C--> 13 <141> CURRENT FILING DATE: 2001-10-03
15 <150> PRIOR APPLICATION NUMBER: 60/251,481
16 <151> PRIOR FILING DATE: 2000-12-05
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1414
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (104)..(1207)
31 <400> SEQUENCE: 1
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34 agcgtggaa ggagcggacc ctgctctccc cgggctgcgg gcc atg gcc acg gcg 115
35 Met Ala Thr Ala
36 1
38 gag cgg aga gcc ctc ggc atc ggc ttc cag tgg ctc tct ttg gcc act 163
39 Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr
40 5 10 15 20
42 ctg gtg ctc atc tgc gcc ggg caa ggg gga cgc agg gag gat ggg ggt 211
43 Leu Val Leu Ile Cys Ala Gly Gln Gly Arg Arg Glu Asp Gly Gly
44 25 30 35
46 cca gcc tgc tac ggc gga ttt gac ctg tac ttc att ttg gac aaa tca 259
47 Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser
48 40 45 50
50 gga agt gtg ctg cac cac tgg aat gaa atc tat tac ttt gtg gaa cag 307
51 Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln
52 55 60 65
54 ttg gct cac aaa ttc atc agc cca cag ttg aga atg tcc ttt att gtt 355
55 Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met Ser Phe Ile Val
56 70 75 80
58 ttc tcc acc cga gga aca acc tta atg aaa ctg aca gaa gac aga gaa 403
59 Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp Arg Glu
60 85 90 95 100
62 cca atc cgt caa ggc cta gaa gaa ctc cag aaa gtt ctg cca gga gga 451
63 Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro Gly Gly
64 105 110 115
66 gac act tac atg cat gaa gga ttt gaa agg gcc agt gag cag att tat 499
67 Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr

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68	120	125	130	
70	tat gaa aac aga caa ggg tac agg aca gcc agc gtc atc att gct ttg			547
71	Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu			
72	135	140	145	
74	act gat gga gaa ctc cat gaa gat ctc ttt ttc tat tca gag agg gag			595
75	Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu			
76	150	155	160	
78	gct aat agg tct cga gat ctt ggt gca att gtt tac tgt gtt ggt gtg			643
79	Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val Gly Val			
80	165	170	175	180
82	aaa gat ttc aat gag aca cag ctg gcc cggtt gct gac agt aag gat			691
83	Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp			
84	185	190	195	
86	cat gtg ttt ccc gtg aat gac ggc ttt cag gct ctg caa ggc atc atc			739
87	His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile			
88	200	205	210	
90	cac tca att ttg aag aag tcc tgc atc gaa att cta gca gct gaa cca			787
91	His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro			
92	215	220	225	
94	tcc acc ata tgt gca gga gag tca ttt caa gtt gtc gtg aga gga aac			835
95	Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg Gly Asn			
96	230	235	240	
98	ggc ttc cga cat gcc cgc aac gtg gac agg gtc ctc tgc agc ttc aag			883
99	Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser Phe Lys			
100	245	250	255	260
102	atc aat gac tcg aca ctc aat gag aag ccc ttt tct gtg gaa gac			931
103	Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ser Val Glu Asp			
104	265	270	275	
106	act tat tta ctg tgt cca gcg cct atc tta aaa gaa gtt ggc atg aaa			979
107	Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly Met Lys			
108	280	285	290	
110	gct gca ctc cag gtc agc atg aac gat ggc ctc tct ttt atc tcc agt			1027
111	Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile Ser Ser			
112	295	300	305	
114	tct gtc atc atc acc acc aca cac tgt tct gac ggt tcc atc ctg gcc			1075
115	Ser Val Ile Ile Thr Thr His Cys Ser Asp Gly Ser Ile Leu Ala			
116	310	315	320	
118	atc gcc ctg ctg atc ctg ttc ctg ctc cta gcc ctg gct ctc ctc tgg			1123
119	Ile Ala Leu Leu Ile Leu Phe Leu Leu Ala Leu Leu Leu Trp			
120	325	330	335	340
122	tgg ttc tgg ccc ctc tgc act gtg att atc aag gag gtc cct cca			1171
123	Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys Glu Val Pro Pro			
124	345	350	355	
126	ccc cct gcc gag gag agt gag gaa aat aaa ata aaa taacaagaag			1217
127	Pro Pro Ala Glu Glu Ser Glu Glu Asn Lys Ile Lys			
128	360	365		
130	aagaaaagaaa gaaatccac agaaacagat aacctaacac agcccgta acgtat tta			1277
132	tacaatgctc tggaaatcat agtctcaatc tagacagtct tttcctctag ttccctgtat			1337
134	tcaaatccca gtgtctaaca ttcaataat agctatatga aatcaaaaaaaa aaaaaaaaaa			1397

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136 aaaaaaaaaa aaaaaaa 1414
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 368
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 2
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148 Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg
149 20 25 30
151 Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile
152 35 40 45
154 Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
155 50 55 60
157 Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
158 65 70 75 80
160 Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
161 85 90 95
163 Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Leu Gln Lys Val
164 100 105 110
166 Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
167 115 120 125
169 Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
170 130 135 140
172 Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
173 145 150 155 160
175 Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
176 165 170 175
178 Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
179 180 185 190
181 Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
182 195 200 205
184 Gln Gly Ile Ile His Ser Ile Leu Lys Ser Cys Ile Glu Ile Leu
185 210 215 220
187 Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
188 225 230 235 240
190 Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
191 245 250 255
193 Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
194 260 265 270
196 Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
197 275 280 285
199 Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
200 290 295 300
202 Phe Ile Ser Ser Ser Val Ile Ile Thr Thr His Cys Ser Asp Gly
203 305 310 315 320
205 Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
206 325 330 335
208 Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys

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209 340 345 350
211 Glu Val Pro Pro Pro Pro Ala Glu Glu Ser Glu Glu Asn Lys Ile Lys
212 355 360 365
216 <210> SEQ ID NO: 3
217 <211> LENGTH: 180
218 <212> TYPE: PRT
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: von Willebrand
223 factor A domain consensus sequence
225 <400> SEQUENCE: 3
226 Pro Leu Asp Val Val Phe Leu Leu Asp Gly Ser Gly Ser Met Gly Gly
227 1 5 10 15
229 Asn Arg Phe Glu Leu Ala Lys Glu Phe Val Leu Lys Leu Val Glu Gln
230 20 25 30
232 Leu Asp Ile Gly Pro Arg Gly Asp Arg Val Gly Leu Val Thr Phe Ser
233 35 40 45
235 Ser Asp Ala Arg Val Leu Phe Pro Leu Asn Asp Ser Gln Ser Lys Asp
236 50 55 60
238 Ala Leu Leu Glu Ala Leu Ala Asn Leu Ser Tyr Ser Leu Gly Gly Gly
239 65 70 75 80
241 Thr Asn Leu Gly Ala Ala Leu Glu Tyr Ala Leu Glu Asn Leu Phe Ser
242 85 90 95
244 Glu Ser Ala Gly Ser Arg Arg Gly Ala Pro Lys Val Leu Ile Leu Ile
245 100 105 110
247 Thr Asp Gly Glu Ser Asn Asp Gly Gly Glu Asp Ile Leu Lys Ala Ala
248 115 120 125
250 Lys Glu Leu Lys Arg Ser Gly Val Lys Val Phe Val Val Gly Val Gly
251 130 135 140
253 Asn Ala Val Asp Glu Glu Leu Lys Lys Leu Ala Ser Ala Pro Gly
254 145 150 155 160
256 Gly Val Phe Ala Val Glu Asp Leu Pro Glu Leu Leu Asp Leu Leu Ile
257 165 170 175
259 Asp Leu Leu Leu
260 180
263 <210> SEQ ID NO: 4
264 <211> LENGTH: 198
265 <212> TYPE: PRT
266 <213> ORGANISM: Homo sapiens
268 <400> SEQUENCE: 4
269 Cys Pro Ser Leu Ile Asp Val Val Val Cys Asp Glu Ser Asn Ser
270 1 5 10 15
272 Ile Tyr Pro Trp Asp Ala Val Lys Asn Phe Leu Glu Lys Phe Val Gln
273 20 25 30
275 Gly Leu Asp Ile Gly Pro Thr Lys Thr Gln Val Gly Leu Ile Gln Tyr
276 35 40 45
278 Ala Asn Asn Pro Arg Val Val Phe Asn Leu Asn Thr Tyr Lys Thr Lys
279 50 55 60
281 Glu Glu Met Ile Val Ala Thr Ser Gln Thr Ser Gln Tyr Gly Gly Asp

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282 65 70 75 80
 284 Leu Thr Asn Thr Phe Gly Ala Ile Gln Tyr Ala Arg Lys Tyr Ala Tyr
 285 85 90 95
 287 Ser Ala Ser Gly Gly Arg Arg Ser Ala Ala Thr Lys Val Met Val Val
 288 100 105 110
 290 Val Thr Asp Gly Glu Ser His Asp Gly Ser Met Leu Lys Ala Val Ile
 291 115 120 125
 293 Asp Gln Cys Asn His Asp Asn Ile Leu Arg Phe Gly Ile Ala Val Leu
 294 130 135 140
 296 Gly Tyr Leu Asn Arg Asn Ala Leu Asp Thr Lys Asn Leu Ile Lys Glu
 297 145 150 155 160
 299 Ile Lys Ala Ile Ala Ser Ile Pro Thr Glu Arg Tyr Phe Phe Asn Val
 300 165 170 175
 302 Ser Asp Glu Ala Ala Leu Leu Glu Lys Ala Gly Thr Leu Gly Glu Gln
 303 180 185 190
 305 Ile Phe Ser Ile Glu Gly
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 309 <210> SEQ ID NO: 5
 310 <211> LENGTH: 5540
 311 <212> TYPE: DNA
 312 <213> ORGANISM: Homo sapiens
 314 <220> FEATURE:
 315 <221> NAME/KEY: CDS
 316 <222> LOCATION: (144)..(1835)
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 321 cgcggatggc gcgtccctga gggtcgtggc gagttcgcgg agcgtggaa ggagcggacc 120
 323 ctgctctccc cgggctgcgg gcc atg gcc acg gcg gag cgg aga gca ctc ggc 173
 324 Met Ala Thr Ala Glu Arg Arg Ala Leu Gly
 325 1 5 10
 327 atc ggc ttc cag tgg ctc tct ttg gcc act ctg gtg ctc atc tgc gcc 221
 328 Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr Leu Val Leu Ile Cys Ala
 329 15 20 25
 331 ggg caa ggg gga cgc agg gag gat ggg ggt cca gcc tgc tac ggc gga 269
 332 Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly
 333 30 35 40
 335 ttt gac ctg tac ttc att ttg gac aaa tca gga agt gtg ctg cac cac 317
 336 Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His
 337 45 50 55
 339 tgg aat gaa atc tat tac ttt gtg gaa cag ttg gct cac aaa ttc atc 365
 340 Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Lys Phe Ile
 341 60 65 70
 343 agc cca cag ttg aga atg tcc ttt att gtt ttc tcc acc cga gga aca 413
 344 Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr
 345 75 80 85 90
 347 acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta 461
 348 Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu
 349 95 100 105
 351 gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa 509

VERIFICATION SUMMARY
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DATE: 10/24/2001
TIME: 14:17:43

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date